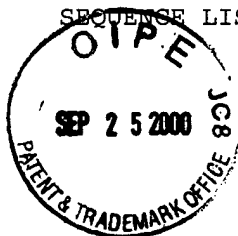


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<120> GENETIC ENGINEERING SALT TOLERANCE IN CROP PLANTS

<130> 1110/0039

<140> PCT/CA99/00219

<141> 1999-03-18

<150> US 60/078,474

<151> 1998-04-01

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<151> 1999-01-15

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<222> (286)..(1899)

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Gln Val Lys Lys Lys Lys Phe Phe His Asn Phe Leu Thr Ile Met Ser 100 105 110		
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Ala Ala Gly Ile Arg Gly Arg Leu Gly His Val Leu Arg Arg His Arg	
	5 10 15
ttc cac tat ctt cct gaa gcc agc ggt tcg ctt ctc att ggt tta atc	153
Phe His Tyr Leu Pro Glu Ala Ser Gly Ser Leu Leu Ile Gly Leu Ile	
	20 25 30
gtc ggt ata ctt gct aat atc tcc gat act gag act agc att agg acg	201
Val Gly Ile Leu Ala Asn Ile Ser Asp Thr Glu Thr Ser Ile Arg Thr	

35	40	45	
tgg ttt aat ttc cac gaa gag ttc ttc ttc ttg ttt ttg ttg cct ccc			249
Trp Phe Asn Phe His Glu Glu Phe Phe Phe Leu Phe Leu Leu Pro Pro			
50	55	60	65
atc ata ttc cag tca ggt ttc agt ctt caa cct aaa cca ttc ttt tct			297
Ile Ile Phe Gln Ser Gly Phe Ser Leu Gln Pro Lys Pro Phe Phe Ser			
	70	75	80
aac ttt gga gcc att gtt acc ttt gct atc atc gga act ttt gtc gct			345
Asn Phe Gly Ala Ile Val Thr Phe Ala Ile Ile Gly Thr Phe Val Ala			
	85	90	95
tca gtt gtt act ggt ggt ctg gtt tat ctt ggc ggc tct atg tat ctc			393
Ser Val Val Thr Gly Gly Leu Val Tyr Leu Gly Gly Ser Met Tyr Leu			
	100	105	110
atg tat aaa ctt ccc ttt gtt gag tgt ctt atg ttt ggt gca ctt ata			441
Met Tyr Lys Leu Pro Phe Val Glu Cys Leu Met Phe Gly Ala Leu Ile			
	115	120	125
tca gct acg gac cct gtc act gta ctc tct ata ttc cag gat gtg ggc			489
Ser Ala Thr Asp Pro Val Thr Val Leu Ser Ile Phe Gln Asp Val Gly			
	130	135	140
acc gat gtt aac ctg tat gct ttg gtc ttt gga gaa tca gtt ctg aat			537
Thr Asp Val Asn Leu Tyr Ala Leu Val Phe Gly Glu Ser Val Leu Asn			
	150	155	160
gat gct atg gca ata tca ttg tac aga aca atg tcc tta gta aac cgc			585
Asp Ala Met Ala Ile Ser Leu Tyr Arg Thr Met Ser Leu Val Asn Arg			
	165	170	175
cag tcc tcg tct ggg gaa cat ttt tca tgggtggtgat cagggtttttt			632
Gln Ser Ser Ser Gly Glu His Phe Ser			
	180	185	
gagactttgc tggctcaatg tcgcaggggt tgggggttgga ttcacttcag cttaatatcc			692
tcctcgatcc tcctattttcc ta			714

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 <213> Arabidopsis thaliana

<220>
 <223> Figure 1(c) (i)

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Arg Phe His Tyr Leu Pro Glu Ala Ser Gly Ser Leu Leu Ile Gly Leu
20 25 30

Ile Val Gly Ile Leu Ala Asn Ile Ser Asp Thr Glu Thr Ser Ile Arg

35					40					45					
Thr	Trp	Phe	Asn	Phe	His	Glu	Glu	Phe	Phe	Phe	Leu	Phe	Leu	Leu	Pro
50			55			60									
Pro	Ile	Ile	Phe	Gln	Ser	Gly	Phe	Ser	Leu	Gln	Pro	Lys	Pro	Phe	Phe
65		70			75			80							
Ser	Asn	Phe	Gly	Ala	Ile	Val	Thr	Phe	Ala	Ile	Ile	Gly	Thr	Phe	Val
85			90			95									
Ala	Ser	Val	Val	Thr	Gly	Gly	Leu	Val	Tyr	Leu	Gly	Gly	Ser	Met	Tyr
100			105			110									
Leu	Met	Tyr	Lys	Leu	Pro	Phe	Val	Glu	Cys	Leu	Met	Phe	Gly	Ala	Leu
115		120			125										
Ile	Ser	Ala	Thr	Asp	Pro	Val	Thr	Val	Leu	Ser	Ile	Phe	Gln	Asp	Val
130		135			140										
Gly	Thr	Asp	Val	Asn	Leu	Tyr	Ala	Leu	Val	Phe	Gly	Glu	Ser	Val	Leu
145		150			155			160							
Asn	Asp	Ala	Met	Ala	Ile	Ser	Leu	Tyr	Arg	Thr	Met	Ser	Leu	Val	Asn
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Arg	Gln	Ser	Ser	Ser	Gly	Glu	His	Phe	Ser						
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 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (52)..(393)
 <223> Figure 1(c)(ii)

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						1		
ggt	cac	ggc	cca	atc	atc	ttt	tac	105
Gly	His	Gly	Pro	Ile	Ile	Phe	Tyr	
	5					10		
acg	gtt	tta	cta	ata	gga	ggt	tcg	153
Thr	Val	Leu	Leu	Ile	Gly	Gly	Ser	
	20				25			
gaa	gtt	gta	ggt	gac	gat	ctt	gat	201
Glu	Val	Val	Gly	Asp	Asp	Leu	Asp	
	35				40			
gag	agc	gat	cat	cag	tat	gtc	cct	249
Glu	Ser	Asp	His	Gln	Tyr	Val	Pro	
				55			60	

tct gac gag gat aca tca tca tca gga agc agg ttc aag atg aag ctg	297
Ser Asp Glu Asp Thr Ser Ser Ser Gly Ser Arg Phe Lys Met Lys Leu	
70 75 80	
aag gag ttt cac aaa acc act aca tca ttc acc gcg ttg gac aaa aac	345
Lys Glu Phe His Lys Thr Thr Thr Ser Phe Thr Ala Leu Asp Lys Asn	
85 90 95	
ttt ctg act ccg ttc ttc aca act aat agt gga gat gga gat gga gat	393
Phe Leu Thr Pro Phe Phe Thr Thr Asn Ser Gly Asp Gly Asp Gly Asp	
100 105 110	
ggggagtagc atggaaaaga tgtgtat	420

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 <211> 114
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 <213> Arabidopsis thaliana

<220>
 <223> Figure 1(c) (ii)

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Thr Arg Gly His Gly Pro Ile Ile Phe Tyr Cys Thr Thr Thr Ile Val	
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Ala Leu Glu Val Val Gly Asp Asp Leu Asp Asp Ser Met Ser Glu Gly	
35 40 45	
Phe Glu Glu Ser Asp His Gln Tyr Val Pro Pro Pro Phe Ser Ile Gly	
50 55 60	
Ala Ser Ser Asp Glu Asp Thr Ser Ser Ser Gly Ser Arg Phe Lys Met	
65 70 75 80	
Lys Leu Lys Glu Phe His Lys Thr Thr Thr Ser Phe Thr Ala Leu Asp	
85 90 95	
Lys Asn Phe Leu Thr Pro Phe Phe Thr Thr Asn Ser Gly Asp Gly Asp	
100 105 110	
Gly Asp	

<210> 9
 <211> 2284
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> Figure 5(a) and (b)

<400> 9

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 ctgtttcggt cctcgtagac gaagaagaag aagaatctca ggttttagct ttcgaagctt 180
 ccaaaatttt gaattttgat cttctgggct cttttgtaaa tcagactgaa gatatttaga 240
 ttaccocagaa gttgttcaag gaatggtttc agtggacagc acggaaagat aaaagagact 300
 tttttttcca gattttgctg atccaaaatc tgaatagttg ttcattgttct tggatcaaat 360
 ctggaaagag gaagtttggt ggatctagaa gaagataaca atgttggatt ctctagtgtc 420
 gaaactgcct tcgttatcga catctgatca cgcttctgtg gttgcgttga atctctttgt 480
 tgcacttctt tgtgcttgta ttgttcttgg tcatcttttg gaagagaata gatggatgaa 540
 cgaatccatc accgccttgt tgattgggct aggcactggg gttaccattt tgttgattag 600
 taaaggaaaa agctcgcac cttctcgtct tagtgaagat cttttcttca tatacttttt 660
 gccaccatt atattcaatg cagggtttca agtaaaaaag aagcagtttt tccgcaattt 720
 cgtgactatt atgctttttg gtgctgttgg gactattatt tcttgacaaa tcatatctct 780
 aggtgtaaca cagttcttta agaagttgga cattggaacc tttgacttgg gtgattatct 840
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ccaactgaga gaaaccctcc tgatcttagt aaggcttgag ggtaacgtgg aagaaaagct 2040
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gtaatatattgt ttgtgaggac agaaatctgt cctaacgttt tgagagcaga aagcaaaaca 2160
tggcaacttt gaagtgtttg attgatgtat gtaattatat tcatatttgt tttgttgtaa 2220
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<210> 10
<211> 547
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<213> Arabidopsis thaliana

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<220>
<223> Figure 5(a)and (b)

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<400> 10

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His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
          20             25             30

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
          35             40             45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
          50             55             60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
 65             70             75             80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
          85             90             95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
          100            105            110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
          115            120            125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
          130            135            140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
          145            150            155            160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
          165            170            175

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Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Val	Phe	180	185	190
Asn	Ala	Ile	Gln	Ser	Phe	Asp	Leu	Thr	His	Leu	Asn	His	Glu	Ala	Ala	195	200	205
Phe	His	Leu	Leu	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Leu	Leu	Ser	Thr	Leu	210	215	220
Leu	Gly	Ala	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Tyr	Val	Ile	Lys	Lys	Leu	225	230	235
Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu	Met	Met	Leu	245	250	255
Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe	Asp	Leu	Ser	Gly	260	265	270
Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser	His	Tyr	Thr	Trp	275	280	285
His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Ile	Thr	Thr	Lys	His	Thr	Phe	Ala	290	295	300
Thr	Leu	Ser	Phe	Leu	Ala	Glu	Thr	Phe	Ile	Phe	Leu	Tyr	Val	Gly	Met	305	310	315
Asp	Ala	Leu	Asp	Ile	Asp	Lys	Trp	Arg	Ser	Val	Ser	Asp	Thr	Pro	Gly	325	330	335
Thr	Ser	Ile	Ala	Val	Ser	Ser	Ile	Leu	Met	Gly	Leu	Val	Met	Val	Gly	340	345	350
Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	Leu	Ala	Lys	355	360	365
Lys	Asn	Gln	Ser	Glu	Lys	Ile	Asn	Phe	Asn	Met	Gln	Val	Val	Ile	Trp	370	375	380
Trp	Ser	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu	Ala	Tyr	Asn	385	390	395
Lys	Phe	Thr	Arg	Ala	Gly	His	Thr	Asp	Val	Arg	Gly	Asn	Ala	Ile	Met	405	410	415
Ile	Thr	Ser	Thr	Ile	Thr	Val	Cys	Leu	Phe	Ser	Thr	Val	Val	Phe	Gly	420	425	430
Met	Leu	Thr	Lys	Pro	Leu	Ile	Ser	Tyr	Leu	Leu	Pro	His	Gln	Asn	Ala	435	440	445
Thr	Thr	Ser	Met	Leu	Ser	Asp	Asp	Asn	Thr	Pro	Lys	Ser	Ile	His	Ile	450	455	460
Pro	Leu	Leu	Asp	Gln	Asp	Ser	Phe	Ile	Glu	Pro	Ser	Gly	Asn	His	Asn	465	470	475
Val	Pro	Arg	Pro	Asp	Ser	Ile	Arg	Gly	Phe	Leu	Thr	Arg	Pro	Thr	Arg	485	490	495

Asn Arg Ala Leu Leu Thr Gly Asp Asn Leu Met Thr Leu Ser Cys Asp
500 505 510

Pro Ser Leu Glu Val Val Ala Leu Tyr Pro Leu Phe Gln Val Leu Gln
515 520 525

Leu Arg Glu Thr Leu Leu Ile Leu Val Arg Leu Glu Gly Asn Val Glu
530 535 540

Glu Lys Leu
545

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<213> Synthetic

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<223> Page 5 and 53 - Forward primer - Isolated
oligonucleotide sequence

<400> 11

gccatgttgg attctctagt gtcg

24

<210> 12

<211> 27

<212> DNA

<213> Synthetic

<220>

<223> Pages 5 and 53 -Reverse primer - isolated
oligonucleotide

<400> 12

ccgaattctc aaagcttttc ttccacg

27

<210> 13

<211> 29

<212> DNA

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<220>

<223> Pages 5 and 53 - Isolated oligonucleotide

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29

<210> 14

<211> 24

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<220>
<223> Page 5 - Isolated oligonucleotide

<400> 14

gccatgttgg attctctagt gtcg 24

<210> 15
<211> 27
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<223> Page 5 - Isolated oligonucleotide

<400> 15

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<400> 16

cggaattcac agaaaaacac agtgaggat 29

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<222> (67)..(1041)
<223> Figure 1(d)

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Met Met Leu Val Leu Ser Phe Val Leu Gly His Val Leu Arg
1 5 10

cgt cat cga ttc cac tat ctt cct gaa gcc agc ggt tcg ctt ctc att 156
Arg His Arg Phe His Tyr Leu Pro Glu Ala Ser Gly Ser Leu Leu Ile
15 20 25 30

ggg tta atc gtc ggt ata ctt gct aat atc tcc gat act gag act agc 204

Gly	Leu	Ile	Val	Gly	Ile	Leu	Ala	Asn	Ile	Ser	Asp	Thr	Glu	Thr	Ser		
				35					40						45		
att	agg	acg	tgg	ttt	aat	ttc	cac	gaa	gag	ttc	ttc	ttc	ttg	ttt	ttg	252	
Ile	Arg	Thr	Trp	Phe	Asn	Phe	His	Glu	Glu	Phe	Phe	Phe	Leu	Phe	Leu		
			50					55					60				
ttg	cct	ccc	atc	ata	ttc	cag	tca	ggg	ttc	agt	ctt	caa	cct	aaa	cca	300	
Leu	Pro	Pro	Ile	Ile	Phe	Gln	Ser	Gly	Phe	Ser	Leu	Gln	Pro	Lys	Pro		
			65				70					75					
ttc	ttt	tct	aac	ttt	gga	gcc	att	gtt	acc	ttt	gct	atc	atc	gga	act	348	
Phe	Phe	Ser	Asn	Phe	Gly	Ala	Ile	Val	Thr	Phe	Ala	Ile	Ile	Gly	Thr		
	80					85					90						
ttt	gtc	gct	tca	gtt	gtt	act	ggg	ggg	ctg	gtt	tat	ctt	ggc	ggc	tct	396	
Phe	Val	Ala	Ser	Val	Val	Thr	Gly	Gly	Leu	Val	Tyr	Leu	Gly	Gly	Ser		
	95				100				105						110		
atg	tat	ctc	atg	tat	aaa	ctt	ccc	ttt	gtt	gag	tgt	ctt	atg	ttt	ggg	444	
Met	Tyr	Leu	Met	Tyr	Lys	Leu	Pro	Phe	Val	Glu	Cys	Leu	Met	Phe	Gly		
				115					120					125			
gca	ctt	ata	tca	gct	acg	gac	cct	gtc	act	gta	ctc	tct	ata	ttc	cag	492	
Ala	Leu	Ile	Ser	Ala	Thr	Asp	Pro	Val	Thr	Val	Leu	Ser	Ile	Phe	Gln		
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gat	gtg	ggc	acc	gat	gtt	aac	ctg	tat	gct	ttg	gtc	ttt	gga	gaa	tca	540	
Asp	Val	Gly	Thr	Asp	Val	Asn	Leu	Tyr	Ala	Leu	Val	Phe	Gly	Glu	Ser		
		145					150					155					
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Val	Leu	Asn	Asp	Ala	Met	Ala	Ile	Ser	Leu	Tyr	Arg	Thr	Met	Ser	Leu		
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Val	Asn	Arg	Gln	Ser	Ser	Ser	Gly	Glu	His	Phe	Phe	Met	Val	Val	Ile		
	175				180					185					190		
agg	ttt	ttt	gag	act	ttt	gct	ggc	tca	atg	tct	gca	ggg	gtt	ggg	gtt	684	
Arg	Phe	Phe	Glu	Thr	Phe	Ala	Gly	Ser	Met	Ser	Ala	Gly	Val	Gly	Val		
				195				200						205			
gga	ttc	act	tca	gct	tta	ctc	ttt	aag	tat	gca	gga	ttg	gac	acc	gag	732	
Gly	Phe	Thr	Ser	Ala	Leu	Leu	Phe	Lys	Tyr	Ala	Gly	Leu	Asp	Thr	Glu		
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Ser	Tyr	Met	Leu	Ala	Glu	Gly	Val	Gly	Leu	Ser	Gly	Ile	Val	Ser	Ile		
	240					245					250						
ctc	ttc	aca	gga	att	gtt	atg	aag	cgc	tac	act	ttc	tca	aat	ctc	tca	876	
Leu	Phe	Thr	Gly	Ile	Val	Met	Lys	Arg	Tyr	Thr	Phe	Ser	Asn	Leu	Ser		
	255				260					265					270		
gaa	gct	tca	cag	agt	ttc	gta	tct	tct	ttt	ttt	cac	ttg	ata	tct	tcg	924	
Glu	Ala	Ser	Gln	Ser	Phe	Val	Ser	Ser	Phe	Phe	His	Leu	Ile	Ser	Ser		

275	280	285	
cta gca gaa act ttc acg ttc att tac atg gga ttt gat att gcc atg			972
Leu Ala Glu Thr Phe Thr Phe Ile Tyr Met Gly Phe Asp Ile Ala Met			
290	295	300	
gag cag cat agc tgg tcc cat gtt ggg ttt atc ctt ttc tct att gta			1020
Glu Gln His Ser Trp Ser His Val Gly Phe Ile Leu Phe Ser Ile Val			
305	310	315	
tcc tca ttt act gat cgt cag tgattgtatg cagtggctgt caatgtattt			1071
Ser Ser Phe Thr Asp Arg Gln			
320	325		
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<213> Arabidopsis thaliana

<220>

<223> Figure 1(d)

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Arg	Phe	His	Tyr	Leu	Pro	Glu	Ala	Ser	Gly	Ser	Leu	Leu	Ile	Gly	Leu
			20					25					30		

Ile	Val	Gly	Ile	Leu	Ala	Asn	Ile	Ser	Asp	Thr	Glu	Thr	Ser	Ile	Arg
		35					40					45			

Thr	Trp	Phe	Asn	Phe	His	Glu	Glu	Phe	Phe	Phe	Leu	Phe	Leu	Leu	Pro
	50					55					60				

Pro Ile Ile Phe Gln Ser Gly Phe Ser Leu Gln Pro Lys Pro Phe Phe

65	70	75	80
Ser Asn Phe Gly Ala Ile Val Thr Phe Ala Ile Ile Gly Thr Phe Val	85	90	95
Ala Ser Val Val Thr Gly Gly Leu Val Tyr Leu Gly Gly Ser Met Tyr	100	105	110
Leu Met Tyr Lys Leu Pro Phe Val Glu Cys Leu Met Phe Gly Ala Leu	115	120	125
Ile Ser Ala Thr Asp Pro Val Thr Val Leu Ser Ile Phe Gln Asp Val	130	135	140
Gly Thr Asp Val Asn Leu Tyr Ala Leu Val Phe Gly Glu Ser Val Leu	145	150	155
Asn Asp Ala Met Ala Ile Ser Leu Tyr Arg Thr Met Ser Leu Val Asn	165	170	175
Arg Gln Ser Ser Ser Gly Glu His Phe Phe Met Val Val Ile Arg Phe	180	185	190
Phe Glu Thr Phe Ala Gly Ser Met Ser Ala Gly Val Gly Val Gly Phe	195	200	205
Thr Ser Ala Leu Leu Phe Lys Tyr Ala Gly Leu Asp Thr Glu Asn Leu	210	215	220
Gln Asn Leu Glu Cys Cys Leu Phe Val Leu Phe Pro Tyr Phe Ser Tyr	225	230	235
Met Leu Ala Glu Gly Val Gly Leu Ser Gly Ile Val Ser Ile Leu Phe	245	250	255
Thr Gly Ile Val Met Lys Arg Tyr Thr Phe Ser Asn Leu Ser Glu Ala	260	265	270
Ser Gln Ser Phe Val Ser Ser Phe Phe His Leu Ile Ser Ser Leu Ala	275	280	285
Glu Thr Phe Thr Phe Ile Tyr Met Gly Phe Asp Ile Ala Met Glu Gln	290	295	300
His Ser Trp Ser His Val Gly Phe Ile Leu Phe Ser Ile Val Ser Ser	305	310	315
Phe Thr Asp Arg Gln	325		

<210> 19

<211> 2122

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (55)..(750)

<223> Figure 1(e) AtNHX4 CDNA sequence

<400> 19

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atg ctc gtg ctt tcc ttc gtt ctc ggc cat gtc ctc cgc cgt cat cga 105
Met Leu Val Leu Ser Phe Val Leu Gly His Val Leu Arg Arg His Arg
                    5                10                15

ttc cac tat ctt cct gaa gcc agc ggt tcg ctt ctc att ggt tta atc 153
Phe His Tyr Leu Pro Glu Ala Ser Gly Ser Leu Leu Ile Gly Leu Ile
                    20                25                30

gtc ggt ata ctt gct aat atc tcc gat act gag act agc att agg acg 201
Val Gly Ile Leu Ala Asn Ile Ser Asp Thr Glu Thr Ser Ile Arg Thr
                    35                40                45

tgg ttt aat ttc cac gaa gag ttc ttc ttc ttg ttt ttg ttg cct ccc 249
Trp Phe Asn Phe His Glu Glu Phe Phe Phe Leu Phe Leu Leu Pro Pro
                    50                55                60                65

atc ata ttc cag tca ggt ttc agt ctt caa cct aaa cca ttc ttt tct 297
Ile Ile Phe Gln Ser Gly Phe Ser Leu Gln Pro Lys Pro Phe Phe Ser
                    70                75                80

aac ttt gga gcc att gtt acc ttt gct atc atc gga act ttt gtc gct 345
Asn Phe Gly Ala Ile Val Thr Phe Ala Ile Ile Gly Thr Phe Val Ala
                    85                90                95

tca gtt gtt act ggt ggt ctg gtt tat ctt ggc ggc tct atg tat ctc 393
Ser Val Val Thr Gly Gly Leu Val Tyr Leu Gly Gly Ser Met Tyr Leu
                    100                105                110

atg tat aaa ctt ccc ttt gtt gag tgt ctt atg ttt ggt gca ctt ata 441
Met Tyr Lys Leu Pro Phe Val Glu Cys Leu Met Phe Gly Ala Leu Ile
                    115                120                125

tca gct acg gac cct gtc act gta ctc tct ata ttc cag gat gtg ggc 489
Ser Ala Thr Asp Pro Val Thr Val Leu Ser Ile Phe Gln Asp Val Gly
                    130                135                140                145

acc gat gtt aac ctg tat gct ttg gtc ttt gga gaa tca gtt ctg aat 537
Thr Asp Val Asn Leu Tyr Ala Leu Val Phe Gly Glu Ser Val Leu Asn
                    150                155                160

gat gct atg gca ata tca ttg tac aga aca atg tcc tta gta aac cgc 585
Asp Ala Met Ala Ile Ser Leu Tyr Arg Thr Met Ser Leu Val Asn Arg
                    165                170                175

cag tcc tcg tct ggg gaa cat ttt ttc atg gtg gtg atc agg ttt ttt 633
Gln Ser Ser Ser Gly Glu His Phe Phe Met Val Val Ile Arg Phe Phe
                    180                185                190

gag act ttt gct ggc tca atg tct gca ggg gtt ggg gtt gga ttc act 681
Glu Thr Phe Ala Gly Ser Met Ser Ala Gly Val Gly Val Gly Phe Thr
                    195                200                205

tca gct tta ata tcc ttc ctc gaa tcc tct att ttt ctt att aga tgt 729
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Ser	Ala	Leu	Ile	Ser	Phe	Leu	Glu	Ser	Ser	Ile	Phe	Leu	Ile	Arg	Cys
210				215				220						225	

cac atg gcc aaa aat gta ttg taaaatctta actcagaaca cctctttaag 780
His Met Ala Lys Asn Val Leu
230

tatgcaggat tggacaccga gaatcttcag aacttggagt gttgtctctt tgtacttttc 840
ccgtatTTTT cgtaagtaga caaaacaact ctctctctgt ctcttcgtat ttatgacaac 900
acttcttccc cctaattgtat tctggttatt ctgtaagata catgcttgca gaaggtgttg 960
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agtagcatgg aaaagatgtg tatttgTggt ccaggccaag ctataattag agtacacata 2040
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gacgatttcc aagacatttc ga 2122

<210> 20
<211> 232
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> Figure 1(e)

<400> 20

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Arg	Phe	His	Tyr	Leu	Pro	Glu	Ala	Ser	Gly	Ser	Leu	Leu	Ile	Gly	Leu
			20					25					30		
Ile	Val	Gly	Ile	Leu	Ala	Asn	Ile	Ser	Asp	Thr	Glu	Thr	Ser	Ile	Arg
		35					40					45			
Thr	Trp	Phe	Asn	Phe	His	Glu	Glu	Phe	Phe	Phe	Leu	Phe	Leu	Leu	Pro
	50					55					60				
Pro	Ile	Ile	Phe	Gln	Ser	Gly	Phe	Ser	Leu	Gln	Pro	Lys	Pro	Phe	Phe
65					70					75					80
Ser	Asn	Phe	Gly	Ala	Ile	Val	Thr	Phe	Ala	Ile	Ile	Gly	Thr	Phe	Val
				85					90					95	
Ala	Ser	Val	Val	Thr	Gly	Gly	Leu	Val	Tyr	Leu	Gly	Gly	Ser	Met	Tyr
			100					105					110		
Leu	Met	Tyr	Lys	Leu	Pro	Phe	Val	Glu	Cys	Leu	Met	Phe	Gly	Ala	Leu
	115						120					125			
Ile	Ser	Ala	Thr	Asp	Pro	Val	Thr	Val	Leu	Ser	Ile	Phe	Gln	Asp	Val
	130					135					140				
Gly	Thr	Asp	Val	Asn	Leu	Tyr	Ala	Leu	Val	Phe	Gly	Glu	Ser	Val	Leu
145					150					155					160
Asn	Asp	Ala	Met	Ala	Ile	Ser	Leu	Tyr	Arg	Thr	Met	Ser	Leu	Val	Asn
			165						170					175	
Arg	Gln	Ser	Ser	Ser	Gly	Glu	His	Phe	Phe	Met	Val	Val	Ile	Arg	Phe
			180					185					190		
Phe	Glu	Thr	Phe	Ala	Gly	Ser	Met	Ser	Ala	Gly	Val	Gly	Val	Gly	Phe
	195					200					205				
Thr	Ser	Ala	Leu	Ile	Ser	Phe	Leu	Glu	Ser	Ser	Ile	Phe	Leu	Ile	Arg
	210					215					220				
Cys	His	Met	Ala	Lys	Asn	Val	Leu								
225					230										

<210> 21
<211> 569
<212> PRT

<213> Schizosaccharomyces pombe

<220>

<223> Figure 8(a)

<400> 21

Met	Pro	Asp	Ser	Lys	His	Trp	Val	Ile	Leu	Leu	Phe	Arg	Arg	Asp	Gly	
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Asp	Asp	Asp	Asp	Asp	Asp	Gly	Gln	Asp	Pro	Ala	Leu	Gln	Glu	Leu	Tyr	
			20					25					30			
Ser	Ser	Trp	Ala	Leu	Phe	Ile	Leu	Leu	Val	Leu	Leu	Ile	Gly	Ala	Leu	
		35					40					45				
Leu	Thr	Ser	Tyr	Tyr	Val	Gln	Ser	Lys	Lys	Ile	Arg	Ala	Ile	His	Glu	
	50					55					60					
Thr	Val	Ile	Ser	Val	Phe	Val	Gly	Met	Val	Val	Gly	Leu	Ile	Ile	Arg	
65					70					75					80	
Val	Ser	Pro	Gly	Leu	Ile	Ile	Gln	Asn	Met	Val	Ser	Phe	His	Ser	Thr	
				85					90					95		
Tyr	Phe	Phe	Asn	Val	Leu	Leu	Pro	Pro	Ile	Ile	Leu	Asn	Ser	Gly	Tyr	
			100					105					110			
Glu	Leu	His	Gln	Ser	Asn	Phe	Phe	Arg	Asn	Ile	Gly	Thr	Ile	Leu	Thr	
		115					120					125				
Phe	Ala	Phe	Ala	Gly	Thr	Phe	Ile	Ser	Ala	Val	Thr	Leu	Gly	Val	Leu	
	130					135					140					
Val	Tyr	Ile	Phe	Ser	Phe	Leu	Asn	Phe	Glu	Asn	Leu	Ser	Met	Thr	Phe	
145					150					155					160	
Val	Glu	Ala	Leu	Ser	Met	Gly	Ala	Thr	Leu	Ser	Ala	Thr	Asp	Pro	Val	
			165						170					175		
Thr	Val	Leu	Ala	Ile	Phe	Asn	Ser	Tyr	Lys	Val	Asp	Gln	Lys	Leu	Tyr	
		180						185					190			
Thr	Ile	Ile	Phe	Gly	Glu	Ser	Ile	Leu	Asn	Asp	Ala	Val	Ala	Ile	Val	
	195						200					205				
Met	Phe	Glu	Thr	Leu	Gln	Gln	Phe	Gln	Gly	Lys	Thr	Leu	His	Phe	Phe	
	210					215					220					
Thr	Leu	Phe	Ser	Gly	Ile	Gly	Ile	Phe	Ile	Ile	Thr	Phe	Phe	Ile	Ser	
225					230					235					240	
Leu	Leu	Ile	Gly	Val	Ser	Ile	Gly	Leu	Ile	Thr	Ala	Leu	Leu	Leu	Lys	
			245						250					255		
Tyr	Ser	Tyr	Leu	Arg	Arg	Tyr	Pro	Ser	Ile	Glu	Ser	Cys	Ile	Ile	Leu	
		260						265					270			
Leu	Met	Ala	Tyr	Thr	Ser	Tyr	Phe	Phe	Ser	Asn	Gly	Cys	His	Met	Ser	
		275					280					285				

Gly Val Val Ser Leu Leu Phe Cys Gly Ile Thr Leu Lys His Tyr Ala
 290 295 300
 Phe Phe Asn Met Ser Tyr Lys Ala Lys Leu Ser Thr Lys Tyr Val Phe
 305 310 315 320
 Arg Val Leu Ala Gln Leu Ser Glu Asn Phe Ile Phe Ile Tyr Leu Gly
 325 330 335
 Met Ser Leu Phe Thr Gln Val Asp Leu Val Tyr Lys Pro Ile Phe Ile
 340 345 350
 Leu Ile Thr Thr Val Ala Val Thr Ala Ser Arg Tyr Met Asn Val Phe
 355 360 365
 Pro Leu Ser Asn Leu Leu Asn Lys Phe His Arg Gln Arg Asn Gly Asn
 370 375 380
 Leu Ile Asp His Ile Pro Tyr Ser Tyr Gln Met Met Leu Phe Trp Ala
 385 390 395 400
 Gly Leu Arg Gly Ala Val Gly Val Ala Leu Ala Ala Gly Phe Glu Gly
 405 410 415
 Glu Asn Ala Gln Thr Leu Arg Ala Thr Thr Leu Val Val Val Val Leu
 420 425 430
 Thr Leu Ile Ile Phe Gly Gly Thr Thr Ala Arg Met Leu Glu Ile Leu
 435 440 445
 His Ile Glu Thr Gly Val Ala Ala Asp Val Asp Ser Asp Thr Glu Ile
 450 455 460
 Gly Met Leu Pro Trp Gln Gln Ser Pro Glu Phe Asp Leu Glu Asn Ser
 465 470 475 480
 Ala Met Glu Leu Ser Asp Ala Ser Ala Glu Pro Val Val Val Asp Gln
 485 490 495
 Gln Phe Thr Thr Glu His Phe Asp Glu Gly Asn Ile Ala Pro Thr Leu
 500 505 510
 Ser Lys Lys Val Ser Ser Thr Phe Glu Gln Tyr Gln Arg Ala Ala Gly
 515 520 525
 Ala Phe Asn Gln Phe Phe His Ser Ser Arg Asp Asp Gln Ala Gln Trp
 530 535 540
 Leu Thr Arg Phe Asp Glu Glu Val Ile Lys Pro Val Leu Leu Glu Arg
 545 550 555 560
 Asp Asn Leu Lys Asn Gly Thr Lys Lys
 565

<210> 22

<211> 633

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<223> Figure 8(b)

<400> 22

Met	Leu	Ser	Lys	Val	Leu	Leu	Asn	Ile	Ala	Phe	Lys	Val	Leu	Leu	Thr	
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Thr	Ala	Lys	Arg	Ala	Val	Asp	Pro	Asp	Asp	Asp	Asp	Glu	Leu	Leu	Pro	
			20					25					30			
Ser	Pro	Asp	Leu	Pro	Gly	Ser	Asp	Asp	Pro	Ile	Ala	Gly	Asp	Pro	Asp	
		35					40					45				
Val	Asp	Leu	Asn	Pro	Val	Thr	Glu	Glu	Met	Phe	Ser	Ser	Trp	Ala	Leu	
	50					55					60					
Phe	Ile	Met	Leu	Leu	Leu	Leu	Ile	Ser	Ala	Leu	Trp	Ser	Ser	Tyr	Tyr	
65					70					75					80	
Leu	Thr	Gln	Lys	Arg	Ile	Arg	Ala	Val	His	Glu	Thr	Val	Leu	Ser	Ile	
				85					90						95	
Phe	Tyr	Gly	Met	Val	Ile	Gly	Leu	Ile	Ile	Arg	Met	Ser	Pro	Gly	His	
			100					105					110			
Tyr	Ile	Gln	Asp	Thr	Val	Thr	Phe	Asn	Ser	Ser	Tyr	Phe	Phe	Asn	Val	
	115						120					125				
Leu	Leu	Pro	Pro	Ile	Ile	Leu	Asn	Ser	Gly	Tyr	Glu	Leu	Asn	Gln	Val	
	130					135					140					
Asn	Phe	Phe	Asn	Asn	Met	Leu	Ser	Ile	Leu	Ile	Phe	Ala	Ile	Pro	Gly	
145					150					155					160	
Thr	Phe	Ile	Ser	Ala	Val	Val	Ile	Gly	Ile	Ile	Leu	Tyr	Ile	Trp	Thr	
				165				170						175		
Phe	Leu	Gly	Leu	Glu	Ser	Ile	Asp	Ile	Ser	Phe	Ala	Asp	Ala	Met	Ser	
			180					185					190			
Val	Gly	Ala	Thr	Leu	Ser	Ala	Thr	Asp	Pro	Val	Thr	Ile	Leu	Ser	Ile	
	195						200					205				
Phe	Asn	Ala	Tyr	Lys	Val	Asp	Pro	Lys	Leu	Tyr	Thr	Ile	Ile	Phe	Gly	
	210					215					220					
Glu	Ser	Leu	Leu	Asn	Asp	Ala	Ile	Ser	Ile	Val	Met	Phe	Glu	Thr	Cys	
225				230						235					240	
Gln	Lys	Phe	His	Gly	Gln	Pro	Ala	Thr	Phe	Ser	Ser	Val	Phe	Glu	Gly	
				245					250				255			
Ala	Gly	Leu	Phe	Leu	Met	Thr	Phe	Ser	Val	Ser	Leu	Leu	Ile	Gly	Val	
			260					265					270			
Leu	Ile	Gly	Ile	Leu	Val	Ala	Leu	Leu	Leu	Lys	His	Thr	His	Ile	Arg	
	275						280					285				

Arg Tyr Pro Gln Ile Glu Ser Cys Leu Ile Leu Leu Ile Ala Tyr Glu
 290 295 300
 Ser Tyr Phe Phe Ser Asn Gly Cys His Met Ser Gly Ile Val Ser Leu
 305 310 315 320
 Leu Phe Cys Gly Ile Thr Leu Lys His Tyr Ala Tyr Tyr Asn Met Ser
 325 330 335
 Arg Arg Ser Gln Ile Thr Ile Lys Tyr Ile Phe Gln Leu Leu Ala Arg
 340 345 350
 Leu Ser Glu Asn Phe Ile Phe Ile Tyr Leu Gly Leu Glu Leu Phe Thr
 355 360 365
 Glu Val Glu Leu Val Tyr Lys Pro Leu Leu Ile Ile Val Ala Ala Ile
 370 375 380
 Ser Ile Cys Val Ala Arg Trp Cys Ala Val Phe Pro Leu Ser Gln Phe
 385 390 395 400
 Val Asn Trp Ile Tyr Arg Val Lys Thr Ile Arg Ser Met Ser Gly Ile
 405 410 415
 Thr Gly Glu Asn Ile Ser Val Pro Asp Glu Ile Pro Tyr Asn Tyr Gln
 420 425 430
 Met Met Thr Phe Trp Ala Gly Leu Arg Gly Ala Val Gly Val Ala Leu
 435 440 445
 Ala Leu Gly Ile Gln Gly Glu Tyr Lys Phe Thr Leu Leu Ala Thr Val
 450 455 460
 Leu Val Val Val Val Leu Thr Val Ile Ile Phe Gly Gly Thr Thr Ala
 465 470 475 480
 Gly Met Leu Glu Val Leu Asn Ile Lys Thr Gly Cys Ile Ser Glu Glu
 485 490 495
 Asp Thr Ser Asp Asp Glu Phe Asp Ile Glu Ala Pro Arg Ala Ile Asn
 500 505 510
 Leu Leu Asn Gly Ser Ser Ile Gln Thr Asp Leu Gly Pro Tyr Ser Asp
 515 520 525
 Asn Asn Ser Pro Asp Ile Ser Ile Asp Gln Phe Ala Val Ser Ser Asn
 530 535 540
 Lys Asn Leu Pro Asn Asn Ile Ser Thr Thr Gly Gly Asn Thr Phe Gly
 545 550 555 560
 Gly Leu Asn Glu Thr Glu Asn Thr Ser Pro Asn Pro Ala Arg Ser Ser
 565 570 575
 Met Asp Lys Arg Asn Leu Arg Asp Lys Leu Gly Thr Ile Phe Asn Ser
 580 585 590
 Asp Ser Gln Trp Phe Gln Asn Phe Asp Glu Gln Val Leu Lys Pro Val
 595 600 605

Phe Leu Asp Asn Val Ser Pro Ser Leu Gln Asp Ser Ala Thr Gln Ser
610 615 620

Pro Ala Asp Phe Ser Ser Gln Asn His
625 630

<210> 23
<211> 378
<212> DNA
<213> Oryza sativa

<220>
<223> Figure 8(c)

<400> 23

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tacaacaaag cagcatttg caactctgtc cttcattgct gagacttttc tcttcctgta 240

tgttgggatg gatgcattgg atattgaaaa atgggagntt nccagtgaca gacctggnaa 300
atccattngg gtaagctcaa ttttgctagg gattggttcc tgattggaag ngctgctttt 360
gnaattcccc tggtggtc                                     378

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<210> 24
<211> 268
<212> DNA
<213> Oryza sativa

<220>
<223> Figure 8 (d)

<400> 24

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gcgaccognc tgcggactac ggctcgatcg cggcgggtggg gatgttcgtg gcgctcatct 120
gcgtctgcat cgctcgtcggc cacctcctcg aggagagccg atggatgaac gagtccatca 180
ccgcgctaata catcgggttg ggtacttgga ggagtnttt tgnatggtgt cgagctggaa 240
gcactcggna tactggtggt cagcgagg                                     268

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<210> 25
<211> 380
<212> DNA
<213> Oryza sativa

<220>
<223> Figure 8(e)

<400> 25

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attgtctggc atcaaactat gccagccac tgatggcacg gctcagttta atgaggctgg 180
ccacaccttc tccagtggga gttatctgtg catctaattg gtaccttctt tgtattgtag 240
ttgttacttt acccttgatt tggtcggttt gcttctaaag caggttgtga aattcctatt 300
gtatgtngtg acgcttggtt gttttttgag gctggaaatt acatcatgtt tttgatttgt 360

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<210> 26

<211> 596

<212> DNA

<213> *Medicago truncatula*

<220>

<223> Figure 8(f)

<400> 26

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aattttattc ttcatatata tatatatata tatccaatta accatctcaa tctcatattc 180
acatatacct cataaaccat ccataacatc cttaaaaaacc ctctaagccc tttcaaactt 240
tgatttgtaa ttgtttctct tataagtctt aacctgcaca aatcaatttt aatttcttat 300
gttcatatag ttatgaatga ttgaaaaaaa cacaaatgac tccagttatc tgtgagatct 360
ctatgataaa ctctactctc cagacgcagg acacatttag ttcaatcttt ctctgttggt 420
ttcctctact gggtctatat tttctcatga attattaatt aatcctatat tctttctttt 480
caatacaaat ttagtttcat taattctatc aacataatca attaaactac atagttagaa 540
aaatagtact attaccacga tcaactcaaag ttttttagtt ttaacaaac antctg 596
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<210> 27

<211> 522

<212> DNA

<213> *Hordeum vulgare*

<220>

<223> Figure 8(g)

<400> 27

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ttccattcag actgatgggt ctggcagaag taatgtattc tgggtggactt acatctatca 120
gcatgatga aacttgatga tcagtttttt tagttgaaaa attctgcaag aacagctact 180
taatgctcta ttgtgtatcg caggcacaca tcagctgctg atgtctgcta tacttctgta 240
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gctagtatgt atactctcac atcatatgct actgttctat atagaactat gtgatagcta 360
ctgctatact gctgtcatac agagtcccgt taatatcaat gctattttgc tttcctcaaa 420
gaaaaaagga aatgactttc cttttgatta tatatttgat ccagggtttc ggcttgctga 480

ctaagcctct gattaatctc ctctgtccac caagacctgg ca 522
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<210> 28

<211> 330

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<223> Figure 8(h)

<400> 28

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aacatgcagg ttgtgatttg gtgggtctgggt ctcattgagag gtgctgtatc tatggctctt 120
gcatacaaca agttttacaag ggccggggcac acagatgtac gnggggaatgc aatcatgac 180
acngntacgn taactgtctg tnttttttagc acagtgggtg ttggtatgct gaccaaacca 240
ntcataagct acctattttac cgnaccanga accgtcatca acngggcatg tttatcttgn 300
attncaaata acccnaanaa tccnatacca 330

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<210> 29

<211> 633

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<223> Figure 2(a)

<400> 29

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Met Leu Ser Lys Val Leu Leu Asn Ile Ala Phe Lys Val Leu Leu Thr
 1              5              10              15

Thr Ala Lys Arg Ala Val Asp Pro Asp Asp Asp Asp Glu Leu Leu Pro
          20              25              30

Ser Pro Asp Leu Pro Gly Ser Asp Asp Pro Ile Ala Gly Asp Pro Asp
          35              40              45

Val Asp Leu Asn Pro Val Thr Glu Glu Met Phe Ser Ser Trp Ala Leu
 50              55              60

Phe Ile Met Leu Leu Leu Leu Ile Ser Ala Leu Trp Ser Ser Tyr Tyr
 65              70              75              80

Leu Thr Gln Lys Arg Ile Arg Ala Val His Glu Thr Val Leu Ser Ile
          85              90              95

Phe Tyr Gly Met Val Ile Gly Leu Ile Ile Arg Met Ser Pro Gly His
          100              105              110

Tyr Ile Gln Asp Thr Val Thr Phe Asn Ser Ser Tyr Phe Phe Asn Val
          115              120              125

Leu Leu Pro Pro Ile Ile Leu Asn Ser Gly Tyr Glu Leu Asn Gln Val
          130              135              140

Asn Phe Phe Asn Asn Met Leu Ser Ile Leu Ile Phe Ala Ile Pro Gly
          145              150              155              160

Thr Phe Ile Ser Ala Val Val Ile Gly Ile Ile Leu Tyr Ile Trp Thr
          165              170              175

Phe Leu Gly Leu Glu Ser Ile Asp Ile Ser Phe Ala Asp Ala Met Ser
          180              185              190

Val Gly Ala Thr Leu Ser Ala Thr Asp Pro Val Thr Ile Leu Ser Ile
          195              200              205

Phe Asn Ala Tyr Lys Val Asp Pro Lys Leu Tyr Thr Ile Ile Phe Gly
          210              215              220

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Glu	Ser	Leu	Leu	Asn	Asp	Ala	Ile	Ser	Ile	Val	Met	Phe	Glu	Thr	Cys	225	230	235	240
Gln	Lys	Phe	His	Gly	Gln	Pro	Ala	Thr	Phe	Ser	Ser	Val	Phe	Glu	Gly	245	250	255	
Ala	Gly	Leu	Phe	Leu	Met	Thr	Phe	Ser	Val	Ser	Leu	Leu	Ile	Gly	Val	260	265	270	
Leu	Ile	Gly	Ile	Leu	Val	Ala	Leu	Leu	Leu	Lys	His	Thr	His	Ile	Arg	275	280	285	
Arg	Tyr	Pro	Gln	Ile	Glu	Ser	Cys	Leu	Ile	Leu	Leu	Ile	Ala	Tyr	Glu	290	295	300	
Ser	Tyr	Phe	Phe	Ser	Asn	Gly	Cys	His	Met	Ser	Gly	Ile	Val	Ser	Leu	305	310	315	320
Leu	Phe	Cys	Gly	Ile	Thr	Leu	Lys	His	Tyr	Ala	Tyr	Tyr	Asn	Met	Ser	325	330	335	
Arg	Arg	Ser	Gln	Ile	Thr	Ile	Lys	Tyr	Ile	Phe	Gln	Leu	Leu	Ala	Arg	340	345	350	
Leu	Ser	Glu	Asn	Phe	Ile	Phe	Ile	Tyr	Leu	Gly	Leu	Glu	Leu	Phe	Thr	355	360	365	
Glu	Val	Glu	Leu	Val	Tyr	Lys	Pro	Leu	Leu	Ile	Ile	Val	Ala	Ala	Ile	370	375	380	
Ser	Ile	Cys	Val	Ala	Arg	Trp	Cys	Ala	Val	Phe	Pro	Leu	Ser	Gln	Phe	385	390	395	400
Val	Asn	Trp	Ile	Tyr	Arg	Val	Lys	Thr	Ile	Arg	Ser	Met	Ser	Gly	Ile	405	410	415	
Thr	Gly	Glu	Asn	Ile	Ser	Val	Pro	Asp	Glu	Ile	Pro	Tyr	Asn	Tyr	Gln	420	425	430	
Met	Met	Thr	Phe	Trp	Ala	Gly	Leu	Arg	Gly	Ala	Val	Gly	Val	Ala	Leu	435	440	445	
Ala	Leu	Gly	Ile	Gln	Gly	Glu	Tyr	Lys	Phe	Thr	Leu	Leu	Ala	Thr	Val	450	455	460	
Leu	Val	Val	Val	Val	Leu	Thr	Val	Ile	Ile	Phe	Gly	Gly	Thr	Thr	Ala	465	470	475	480
Gly	Met	Leu	Glu	Val	Leu	Asn	Ile	Lys	Thr	Gly	Cys	Ile	Ser	Glu	Glu	485	490	495	
Asp	Thr	Ser	Asp	Asp	Glu	Phe	Asp	Ile	Glu	Ala	Pro	Arg	Ala	Ile	Asn	500	505	510	
Leu	Leu	Asn	Gly	Ser	Ser	Ile	Gln	Thr	Asp	Leu	Gly	Pro	Tyr	Ser	Asp	515	520	525	
Asn	Asn	Ser	Pro	Asp	Ile	Ser	Ile	Asp	Gln	Phe	Ala	Val	Ser	Ser	Asn	530	535	540	

Lys Asn Leu Pro Asn Asn Ile Ser Thr Thr Gly Gly Asn Thr Phe Gly
 545 550 555 560
 Gly Leu Asn Glu Thr Glu Asn Thr Ser Pro Asn Pro Ala Arg Ser Ser
 565 570 575
 Met Asp Lys Arg Asn Leu Arg Asp Lys Leu Gly Thr Ile Phe Asn Ser
 580 585 590
 Asp Ser Gln Trp Phe Gln Asn Phe Asp Glu Gln Val Leu Lys Pro Val
 595 600 605
 Phe Leu Asp Asn Val Ser Pro Ser Leu Gln Asp Ser Ala Thr Gln Ser
 610 615 620
 Pro Ala Asp Phe Ser Ser Gln Asn His
 625 630

 <210> 30
 <211> 669
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> Figure 2(a) HsNHE6 Na⁺/H⁺ exchanger (GenBank
 Accession No. 2944237)

 <400> 30
 Met Ala Arg Arg Gly Trp Arg Arg Ala Pro Leu Arg Arg Gly Val Gly
 1 5 10 15
 Ser Ser Pro Arg Ala Arg Arg Leu Met Arg Pro Leu Trp Leu Leu Leu
 20 25 30

 Ala Val Gly Val Phe Asp Trp Ala Gly Ala Ser Asp Gly Gly Gly Gly
 35 40 45
 Glu Ala Arg Ala Met Asp Glu Glu Ile Val Ser Glu Lys Gln Ala Glu
 50 55 60
 Glu Ser His Arg Gln Asp Ser Ala Asn Leu Leu Ile Phe Ile Leu Leu
 65 70 75 80
 Leu Thr Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys His Arg Arg Ala
 85 90 95
 Arg Phe Leu His Glu Thr Gly Leu Ala Met Ile Tyr Gly Leu Leu Val
 100 105 110
 Gly Leu Val Leu Arg Tyr Gly Ile His Val Pro Ser Asp Val Asn Asn
 115 120 125
 Val Thr Leu Ser Cys Glu Val Gln Ser Ser Pro Thr Thr Leu Leu Val
 130 135 140
 Thr Phe Asp Pro Glu Val Phe Phe Asn Ile Leu Leu Pro Pro Ile Ile
 145 150 155 160

Phe Tyr Ala Gly Tyr Ser Leu Lys Arg Arg His Phe Phe Arg Asn Leu
165 170 175
Gly Ser Ile Leu Ala Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Phe
180 185 190
Val Ile Gly Ser Ile Met Tyr Gly Cys Val Thr Leu Met Lys Val Thr
195 200 205
Gly Gln Leu Ala Gly Asp Phe Tyr Phe Thr Asp Cys Leu Leu Phe Gly
210 215 220
Ala Ile Val Ser Ala Thr Asp Pro Val Thr Val Leu Ala Ile Phe His
225 230 235 240
Glu Leu Gln Val Asp Val Glu Leu Tyr Ala Leu Leu Phe Gly Glu Ser
245 250 255
Val Leu Asn Asp Ala Val Ala Ile Val Leu Ser Ser Ser Ile Val Ala
260 265 270
Tyr Gln Pro Ala Gly Asp Asn Ser His Thr Phe Asp Val Thr Ala Met
275 280 285
Phe Lys Ser Ile Gly Ile Phe Leu Gly Ile Phe Ser Gly Ser Phe Ala
290 295 300
Met Gly Ala Ala Thr Gly Val Val Thr Ala Leu Val Thr Lys Phe Thr
305 310 315 320
Lys Leu Arg Glu Phe Gln Leu Leu Glu Thr Gly Leu Phe Phe Leu Met
325 330 335
Ser Trp Ser Thr Phe Leu Leu Ala Glu Ala Trp Gly Phe Thr Gly Val
340 345 350
Val Ala Val Leu Phe Cys Gly Ile Thr Gln Ala His Tyr Thr Tyr Asn
355 360 365
Asn Leu Ser Thr Glu Ser Gln His Arg Thr Lys Gln Leu Phe Glu Leu
370 375 380
Leu Asn Phe Leu Ala Glu Asn Phe Ile Phe Ser Tyr Met Gly Leu Thr
385 390 395 400
Leu Phe Thr Phe Gln Asn His Val Phe Asn Pro Thr Phe Val Val Gly
405 410 415
Ala Phe Val Ala Ile Phe Leu Gly Arg Ala Ala Asn Ile Tyr Pro Leu
420 425 430
Ser Leu Leu Leu Asn Leu Gly Arg Arg Ser Lys Ile Gly Ser Asn Phe
435 440 445
Gln His Met Met Met Phe Ala Gly Leu Arg Gly Ala Met Ala Phe Ala
450 455 460
Leu Ala Ile Arg Asp Thr Ala Thr Tyr Ala Arg Gln Met Met Phe Ser
465 470 475 480
Thr Thr Leu Leu Ile Val Phe Phe Thr Val Trp Val Phe Gly Gly Gly

485					490					495					
Thr	Thr	Ala	Met	Leu	Ser	Cys	Leu	His	Ile	Arg	Val	Gly	Val	Asp	Ser
			500					505					510		
Asp	Gln	Glu	His	Leu	Gly	Val	Pro	Glu	Asn	Glu	Arg	Arg	Thr	Thr	Lys
			515				520					525			
Ala	Glu	Ser	Ala	Trp	Leu	Phe	Arg	Met	Trp	Tyr	Asn	Phe	Asp	His	Asn
			530				535					540			
Tyr	Leu	Lys	Pro	Leu	Leu	Thr	His	Ser	Gly	Pro	Pro	Leu	Thr	Thr	Thr
			545				550					555			560
Leu	Pro	Ala	Cys	Cys	Gly	Pro	Ile	Ala	Arg	Cys	Leu	Thr	Ser	Pro	Gln
				565					570					575	
Ala	Tyr	Glu	Asn	Gln	Glu	Gln	Leu	Lys	Asp	Asp	Asp	Ser	Asp	Leu	Ile
			580					585					590		
Leu	Asn	Asp	Gly	Asp	Ile	Ser	Leu	Thr	Tyr	Gly	Asp	Ser	Thr	Val	Asn
			595				600					605			
Thr	Glu	Pro	Ala	Thr	Ser	Ser	Ala	Pro	Arg	Arg	Phe	Met	Gly	Asn	Ser
			610				615					620			
Ser	Glu	Asp	Ala	Leu	Asp	Arg	Glu	Leu	Ala	Phe	Gly	Asp	His	Glu	Leu
			625				630					635			640
Val	Ile	Arg	Gly	Thr	Arg	Leu	Val	Leu	Pro	Met	Asp	Asp	Ser	Glu	Pro
				645					650					655	
Pro	Leu	Asn	Leu	Leu	Asp	Asn	Thr	Arg	His	Gly	Pro	Ala			
			660					665							

<210> 31

<211> 541

<212> PRT

<213> C. elegans

<220>

<223> Figure 2(a) CeNHE1 (GenBank Accession No. 3877723)

<400> 31

Met	Lys	Val	Glu	Ser	Leu	Phe	Phe	Met	Ser	Gln	Thr	Phe	Asp	Val	Ile
1				5					10					15	
Thr	Lys	Asn	Lys	Thr	Ile	Val	Lys	Glu	Pro	Pro	Asp	Tyr	Leu	Met	Leu
			20					25					30		
Glu	Val	Lys	Pro	Glu	Gly	Gly	Ser	Arg	Val	Ser	Phe	His	Tyr	Glu	Leu
			35				40					45			
Ile	Glu	Gly	Phe	Phe	Ala	Asp	Lys	Arg	Lys	Lys	Ile	Glu	Gln	Gln	Ile
			50				55				60				
Glu	Gln	Lys	Ser	Val	Phe	Ser	Pro	Glu	Val	Phe	Phe	Asn	Met	Leu	Ile
			65			70				75				80	

Pro Pro Ile Ile Phe Asn Ala Gly Tyr Ser Leu Lys Lys Arg His Phe
 85 90 95

Phe Arg Asn Ile Gly Ser Ile Leu Ala Ile Val Phe Ile Gly Thr Thr
 100 105 110

Ile Ser Cys Phe Gly Thr Gly Cys Leu Met Phe Val Phe Thr Ser Ile
 115 120 125

Phe Gln Met Gly Tyr Ser Phe Lys Glu Leu Leu Phe Phe Gly Ala Leu
 130 135 140

Ile Ser Ala Thr Asp Pro Val Thr Ile Ile Ser Val Phe Asn Asp Met
 145 150 155 160

Asn Val Glu Ala Asp Leu Phe Ala Leu Ile Phe Gly Glu Ser Ala Leu
 165 170 175

Asn Asp Ala Val Ala Ile Val Leu Ser Glu Val Ile Glu Asn Phe Ser
 180 185 190

Thr Ser Ser Glu Ala Ile Thr Leu Gln Asp Phe Gly Ser Ala Ile Ala
 195 200 205

Gly Phe Ala Gly Val Phe Phe Gly Ser Leu Met Leu Gly Phe Met Ile
 210 215 220

Gly Cys Met Asn Ala Phe Leu Thr Lys Met Thr Leu Ile Ser Glu His
 225 230 235 240

Ala Leu Leu Glu Ser Ser Leu Phe Val Leu Ile Ser Tyr Ile Ser Phe
 245 250 255

Leu Val Ala Glu Val Cys Gly Leu Thr Gly Ile Val Ser Val Leu Phe
 260 265 270

Cys Gly Ile Ala Gln Ala His Tyr Thr Tyr Asn Asn Leu Ser Asp Glu
 275 280 285

Ser Gln Ser Asn Thr Lys His Phe Phe His Met Val Ser Phe Ile Met
 290 295 300

Glu Ser Phe Ile Phe Cys Tyr Ile Gly Val Ser Val Phe Val Thr Asn
 305 310 315 320

Asn Gln Arg Trp Ser Phe Ser Phe Leu Leu Phe Ser Leu Ile Ser Ile
 325 330 335

Thr Ala Ser Arg Ala Leu Phe Val Tyr Pro Leu Ser Trp Leu Leu Asn
 340 345 350

Ile Arg Arg Arg Pro Lys Ile Pro Lys Arg Tyr Gln His Met Ile Leu
 355 360 365

Phe Ala Gly Leu Arg Gly Ala Met Ala Phe Ala Leu Ala Gly Arg Asn
 370 375 380

Thr Ser Thr Glu Asn Arg Gln Met Ile Phe Ala Thr Thr Thr Ala Val
 385 390 395 400

Val Ile Val Thr Val Leu Val Asn Gly Gly Leu Thr Ser Trp Met Ile
 405 410 415
 Asp Tyr Leu Gln Ile Lys His Gly Lys Asp Ala Ile Glu Glu Gly Gln
 420 425 430
 Arg Leu Glu Asn Ser Met Ser Ser Ser Pro Ala Asp Gln His Ser Asp
 435 440 445
 Leu Asp Glu Ser Val Pro Val Thr Met Ser Pro Gly Leu Asn Pro Trp
 450 455 460
 Asp Lys Ala Phe Leu Pro Arg Lys Trp Tyr His Phe Asp Ala Arg Trp
 465 470 475 480
 Gln Leu Leu Lys Leu Val Phe Gln Phe His Glu Thr Ser Thr Asp Pro
 485 490 495
 Cys Asp Ala Ile Phe Gly Thr Asn Thr Pro Thr Val Leu Ser Ser Ile
 500 505 510
 Asp Phe Leu Val Asp Phe Lys Pro Ser Thr Arg Val Arg Gln Cys Arg
 515 520 525
 Ala Leu Gln Tyr Asn Cys Thr Ile Arg Asp Ser Ile Asp
 530 535 540

<210> 32
 <211> 21
 <212> DNA
 <213> Synthetic

<220>
 <223> Page 54 - PCR forward primer (X6F)

<400> 32

cctcaggtga taccaatctc a

21

<210> 33
 <211> 20
 <212> DNA
 <213> Synthetic

<220>
 <223> Page 54 - PCR reverse primer (X6REV)

<400> 33

gatccaatgt aacaccggag

20

<210> 34
 <211> 19
 <212> DNA
 <213> Synthetic

<220>
 <223> Page 54 - PCR forward primer (NHX7F)
 <400> 34
 ttcggttctcg gccatgtcc 19
 <210> 35
 <211> 22
 <212> DNA
 <213> Synthetic
 <220>
 <223> Page 54 - PCR reverse primer (NHX7REV)
 <400> 35
 cggagagacc aacaccttct gc 22
 <210> 36
 <211> 24
 <212> DNA
 <213> Synthetic
 <220>
 <223> Page 37 - preferred oligonucleotide probe
 <400> 36
 ttcttcatat atcttttgcc accc 24
 <210> 37
 <211> 30
 <212> DNA
 <213> Synthetic
 <220>
 <223> Page 55 - Primer
 <400> 37
 cgcgtcgaca tggtggattc tctagtgtcg 30
 1
 37/37